



SEQUENCE LISTING

<110> Bristol-Myers Squibb Company
<120> AGGRECAN DEGRADING METALLO PROTEASES
<130> DM6909B
<140> US/09/634,287
<141> 2000-08-09
<160> 21
<170> PatentIn version 3.0
<210> 1
<211> 4192
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (406)..(2916)

<400> 1
acagacacat atgcacgaga gagacagagg aggaagaga cagagacaaa ggcacagcgg 60
aagaaggcag agacagggca ggcacagaag cggcccagac agagtcctac agagggagag 120
gccagagaag ctgcagaaga cacaggcagg gagagacaaa gatccaggaa aggagggctc 180
aggaggagag tttggagaag ccagaccctt gggcacctct cccaagccca aggactaagt 240
tttctccatt tcctttaacg gtcttcagcc cttctgaaaa ctttgcctct gaccttggca 300
ggagtccaag cccccaggct acagagagga gctttccaaa gctagggtgt ggaggacttg 360
gtgccctaga cggcctcagt cctcaccagc tgcagtacca gtgcc atg tcc cag aca 417
Met Ser Gln Thr
1
ggc tcg cat ccc ggg agg ggc ttg gca ggg cgc tgg ctg tgg gga gcc 465
Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg Trp Leu Trp Gly Ala
5 10 15 20
caa ccc tgc ctc ctg ctc ccc att gtg cgc ptc tcc tgg ctg gtg tgg 513
Gln Pro Cys Leu Leu Leu Pro Ile Val Pro Leu Ser Trp Leu Val Trp
25 30 35
ctg ctt ctg cta ctg ctg gcc tct ctc ctg ccc tca gcc cgg ctg gcc 561

RECEIVED

JUL 29 2002

TECH CENTER 1600/2900

INS
D2

CT

Leu Leu Leu Leu Leu Leu Ala Ser Leu Leu Pro Ser Ala Arg Leu Ala
 40 45 50

agc ccc ctc ccc cgg gag gag gag atc gtg ttt cca gag aag ctc aac 609
 Ser Pro Leu Pro Arg Glu Glu Glu Ile Val Phe Pro Glu Lys Leu Asn
 55 60 65

ggc agc gtc ctg cct ggc tcg ggc gcc cct gcc agg ctg ttg tgc cgc 657
 Gly Ser Val Leu Pro Gly Ser Gly Ala Pro Ala Arg Leu Leu Cys Arg
 70 75 80

ttg cag gcc ttt ggg gag acg ctg cta cta gag ctg gag cag gac tcc 705
 Leu Gln Ala Phe Gly Glu Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser
 85 90 95 100

ggt gtg cag gtc gag ggg ctg aca gtg cag tac ctg ggc cag gcg cct 753
 Gly Val Gln Val Glu Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro
 105 110 115

gag ctg ctg ggt gga gca gag cct ggc acc tac ctg act ggc acc atc 801
 Glu Leu Leu Gly Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile
 120 125 130

aat gga gat ccg gag tcg gtg gca tct ctg cac tgg gat ggg gga gcc 849
 Asn Gly Asp Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala
 135 140 145

ctg tta ggc gtg tta caa tat cgg ggg gct gaa ctc cac ctc cag ccc 897
 Leu Leu Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro
 150 155 160

ctg gag gga ggc acc cct aac tct gct ggg gga cct ggg gct cac atc 945
 Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile
 165 170 175 180

cta cgc cgg aag agt cct gcc agc ggt caa ggt ccc atg tgc aac gtc 993
 Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn Val
 185 190 195

aag gct cct ctt gga agc ccc agc ccc aga ccc aga gga gcc aag cgc 1041
 Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala Lys Arg
 200 205 210

ttt gct tca ctg agt aga ttt gtg gag aca ctg gtg gtg gca gat gac 1089
 Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val Ala Asp Asp
 215 220 225

aag atg gcc gca ttc cac ggt gcg ggg cta aag cgc tac ctg cta aca 1137
 Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg Tyr Leu Leu Thr
 230 235 240

gtg atg gca gca gca gcc aag gcc ttc aag cac cca agc atc cgc aat 1185
 Val Met Ala Ala Ala Ala Lys Ala Phe Lys His Pro Ser Ile Arg Asn
 245 250 255 260

cct gtc agc ttg gtg gtg act cgg cta gtg atc ctg ggg tca ggc gag 1233
 Pro Val Ser Leu Val Val Thr Arg Leu Val Ile Leu Gly Ser Gly Glu

C1

265

270

275

gag ggg ccc caa gtg ggg ccc agt gct gcc cag acc ctg cgc agc ttc 1281
 Glu Gly Pro Gln Val Gly Pro Ser Ala Ala Gln Thr Leu Arg Ser Phe
 280 285 290

tgt gcc tgg cag cgg ggc ctc aac acc cct gag gac tcg gac cct gac 1329
 Cys Ala Trp Gln Arg Gly Leu Asn Thr Pro Glu Asp Ser Asp Pro Asp
 295 300 305

cac ttt gac aca gcc att ctg ttt acc cgt cag gac ctg tgt gga gtc 1377
 His Phe Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Val
 310 315 320

tcc act tgc gac acg ctg ggt atg gct gat gtg ggc acc gtc tgt gac 1425
 Ser Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp
 325 330 335 340

ccg gct cgg agc tgt gcc att gtg gag gat gat ggg ctc cag tca gcc 1473
 Pro Ala Arg Ser Cys Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala
 345 350 355

ttc act gct gct cat gaa ctg ggt cat gtc ttc aac atg ctc cat gac 1521
 Phe Thr Ala Ala His Glu Leu Gly His Val Phe Asn Met Leu His Asp
 360 365 370

C1 aac tcc aag cca tgc atc agt ttg aat ggg cct ttg agc acc tct cgc 1569
 Asn Ser Lys Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg
 375 380 385

cat gtc atg gcc cct gtg atg gct cat gtg gat cct gag gag ccc tgg 1617
 His Val Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp
 390 395 400

tcc ccc tgc agt gcc cgc ttc atc act gac ttc ctg gac aat ggc tat 1665
 Ser Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr
 405 410 415 420

ggg cac tgt ctc tta gac aaa cca gag gct cca ttg cat ctg cct gtg 1713
 Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro Val
 425 430 435

act ttc cct ggc aag gac tat gat gct gac cgc cag tgc cag ctg acc 1761
 Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln Leu Thr
 440 445 450

ttc ggg ccc gac tca cgc cat tgt cca cag ctg ccg ccg acc tgt gct 1809
 Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro Pro Cys Ala
 455 460 465

gcc ctc tgg tgc tct ggc cac ctc aat ggc cat gcc atg tgc cag acc 1857
 Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala Met Cys Gln Thr
 470 475 480

aaa cac tcg ccc tgg gcc gat ggc aca ccc tgc ggg ccc gca cag gcc 1905
 Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys Gly Pro Ala Gln Ala
 485 490 495 500

tgc atg ggt ggt cgc tgc ctc cac atg gac cag ctc cag gac ttc aat 1953
 Cys Met Gly Gly Arg Cys Leu His Met Asp Gln Leu Gln Asp Phe Asn
 505 510 515

att cca cag gct ggt ggc tgg ggt cct tgg gga cca tgg ggt gac tgc 2001
 Ile Pro Gln Ala Gly Gly Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys
 520 525 530

tct cgg acc tgt ggg ggt ggt gtc cag ttc tcc tcc cga gac tgc acg 2049
 Ser Arg Thr Cys Gly Gly Gly Val Gln Phe Ser Ser Arg Asp Cys Thr
 535 540 545

agg cct gtc ccc cgg aat ggt ggc aag tac tgt gag ggc cgc cgt acc 2097
 Arg Pro Val Pro Arg Asn Gly Gly Lys Tyr Cys Glu Gly Arg Arg Thr
 550 555 560

cgc ttc cgc tcc tgc aac act gag gac tgc cca act ggc tca gcc ctg 2145
 Arg Phe Arg Ser Cys Asn Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu
 565 570 575 580

acc ttc cgc gag gag cag tgt gct gcc tac aac cac cgc acc gac ctc 2193
 Thr Phe Arg Glu Glu Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu
 585 590 595

ttc aag agc ttc cca ggg ccc atg gac tgg gtt cct cgc tac aca ggc 2241
 Phe Lys Ser Phe Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly
 600 605 610

gtg gcc ccc cag gac cag tgc aaa ctc acc tgc cag gcc cgg gca ctg 2289
 Val Ala Pro Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu
 615 620 625

ggc tac tac tat gtg ctg gag cca cgg gtg gta gat ggg acc ccc tgt 2337
 Gly Tyr Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys
 630 635 640

tcc ccg gac agc tcc tcg gtc tgt gtc cag ggc cga tgc atc cat gct 2385
 Ser Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
 645 650 655 660

ggc tgt gat cgc atc att ggc tcc aag aag aag ttt gac aag tgc atg 2433
 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys Met
 665 670 675

gtg tgc gga ggg gac ggt tct ggt tgc agc aag cag tca ggc tcc ttc 2481
 Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly Ser Phe
 680 685 690

agg aaa ttc agg tac gga tac aac aat gtg gtc act atc ccc gag ggg 2529
 Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile Pro Ala Gly
 695 700 705

gcc acc cac att ctt gtc cgg cag cag gga aac cct ggc cac cgg agc 2577
 Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro Gly His Arg Ser
 710 715 720

atc tac ttg gcc ctg aag ctg cca gat ggc tcc tat gcc ctc aat ggt 2625
 Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser Tyr Ala Leu Asn Gly
 725 730 735 740
 gaa tac acg ctg atg ccc tcc ccc aca gat gtg gta ctg cct ggg gca 2673
 Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp Val Val Leu Pro Gly Ala
 745 750 755
 gtc agc ttg cgc tac agc ggg gcc act gca gcc tca gag aca ctg tca 2721
 Val Ser Leu Arg Tyr Ser Gly Ala Thr Ala Ala Ser Glu Thr Leu Ser
 760 765 770
 ggc cat ggg cca ctg gcc cag cct ttg aca ctg caa gtc cta gtg gct 2769
 Gly His Gly Pro Leu Ala Gln Pro Leu Thr Leu Gln Val Leu Val Ala
 775 780 785
 ggc aac ccc cag gac aca cgc ctc cga tac agc ttc ttc gtg ccc cgg 2817
 Gly Asn Pro Gln Asp Thr Arg Leu Arg Tyr Ser Phe Phe Val Pro Arg
 790 795 800
 ccg acc cct tca acg cca cgc ccc act ccc cag gac tgg ctg cac cga 2865
 Pro Thr Pro Ser Thr Pro Arg Pro Thr Pro Gln Asp Trp Leu His Arg
 805 810 815 820
 aga gca cag att ctg gag atc ctt cgg cgg cgc ccc tgg gcg ggc agg 2913
 Arg Ala Gln Ile Leu Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg
 825 830 835
 aaa taacctcact atccccggctg ccctttcttg gcaccggggc ctccggactta 2966
 Lys
 gctgggagaa agagagagct tctgttgctg cctcatgcta agactcagtg gggaggggct 3026
 gtgggcgtga gacctgcccc tctctctctgc cctaatagcgc aggctggccc tgccctggtt 3086
 tctgcccctg ggaggcagtg atgggttagt ggatggaagg gactgacaga cagccctcca 3146
 tctaaactgc cccctctgcc ctgcgggtca caggaggag ggggaaggca gggagggcct 3206
 gggccccagt tgtatttatt tagtatttat tcacttttat ttagcaaccag ggaaggggac 3266
 aaggactagg gtccctgggga acctgacccc tgacccctca tagccctcac cctgggggcta 3326
 ggaaatccag ggtggtggtg ataggtataa gtggtgtgtg tatgcgtgtg tgtgtgtgtg 3386
 tgaaaatgtg tgtgtgctta tgtatgaggt acaacctgtt ctgctttcct ctccctgaat 3446
 tttatttttt gggaaaagaa aagtcaaggg taggggtggc cttcaggag tgagggatta 3506
 tccttttttt tttctttctt tctttctttt tttttttgag acagaatctc gctctgtcgc 3566
 ccaggctgga gtgcaatggc acaatctcgg ctactgcat cctccgcctc ccgggttcaa 3626
 gtgattctca tgccctagcc tcttgagtag ctgggattac aggtccctgc caccacgccc 3686
 ggctaatttt tgttttggtt tgtttgagaga cagagtctcg ctattgtcac cagggctgga 3746

atgatttcag ctcaactgcaa ccttcgccac ctgggttcca gcaattctcc tgcctcagcc 3806
 tcccagtag ctgagattat aggcacctac caccacgccc ggctaatttt tgtattttta 3866
 gtagagacgg ggtttcacca tgttggccag gctgggtctcg aactcctgac cttaggtgat 3926
 ccactcgct tcacttccca aagtgtggg attacaggcg tgagccaccg tgcctggcca 3986
 cgcccaacta atttttgtat ttttagtaga gacagggttt caccatgttg gccaggctgc 4046
 tcttgaactc ctgacctcag gtaatcgacc tgcctcggcc tcccaaagtg ctgggattac 4106
 aggtgtgagc caccacgccc ggtacatatt ttttaaattg aattctacta tttatgtgat 4166
 ccttttggag tcagacagat gtgggt 4192

<210> 2

<211> 837

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg Trp
 1 5 10 15
 Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro Leu Ser
 20 25 30
 Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu Leu Pro Ser
 35 40 45
 Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu Ile Val Phe Pro
 50 55 60
 Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser Gly Ala Pro Ala Arg
 65 70 75 80
 Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu Thr Leu Leu Leu Glu Leu
 85 90 95
 Glu Gln Asp Ser Gly Val Gln Val Glu Gly Leu Thr Val Gln Tyr Leu
 100 105 110
 Gly Gln Ala Pro Glu Leu Leu Gly Gly Ala Glu Pro Gly Thr Tyr Leu
 115 120 125
 Thr Gly Thr Ile Asn Gly Asp Pro Glu Ser Val Ala Ser Leu His Trp
 130 135 140
 Asp Gly Gly Ala Leu Leu Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu
 145 150 155 160

His Leu Gln Pro Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro
 165 170 175
 Gly Ala His Ile Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro
 180 185 190
 Met Cys Asn Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg
 195 200 205
 Arg Ala Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val
 210 215 220
 Val Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg
 225 230 235 240
 Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His Pro
 245 250 255
 Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val Ile Leu
 260 265 270
 Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala Ala Gln Thr
 275 280 285
 Leu Arg Ser Phe Cys Ala Tyr Gln Arg Gly Leu Asn Thr Pro Glu Asp
 290 295 300
 Ser Asp Pro Asp His Phe Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp
 305 310 315 320
 Leu Cys Gly Val Ser Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly
 325 330 335
 Thr Val Cys Asp Pro Ala Arg Ser Cys Ala Ile Val Glu Asp Asp Gly
 340 345 350
 Leu Gln Ser Ala Phe Thr Ala Ala His Glu Leu Gly His Val Phe Asn
 355 360 365
 Met Leu His Asp Asn Ser Lys Pro Cys Ile Ser Leu Asn Gly Pro Leu
 370 375 380
 Ser Thr Ser Arg His Val Met Ala Pro Val Met Ala His Val Asp Pro
 385 390 395 400
 Glu Glu Pro Trp Ser Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu
 405 410 415
 Asp Asn Gly Tyr Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu
 420 425 430
 His Leu Pro Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln
 435 440 445
 Cys Gln Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro
 450 455 460

C1

Pro Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
 465 470 475 480
 Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys Gly
 485 490 495
 Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp Gln Leu
 500 505 510
 Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro Trp Gly Pro
 515 520 525
 Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Gln Phe Ser Ser
 530 535 540
 Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly Gly Lys Tyr Cys Glu
 545 550 555 560
 Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn Thr Glu Asp Cys Pro Thr
 565 570 575
 Gly Ser Ala Leu Thr Phe Arg Glu Glu Gln Cys Ala Ala Tyr Asn His
 580 585 590
 Arg Thr Asp Leu Phe Lys Ser Phe Pro Gly Pro Met Asp Trp Val Pro
 595 600 605
 Arg Tyr Thr Gly Val Ala Pro Gln Asp Gln Cys Lys Leu Thr Cys Gln
 610 615 620
 Ala Arg Ala Leu Gly Tyr Tyr Tyr Val Leu Glu Pro Arg Val Val Asp
 625 630 635 640
 Gly Thr Pro Cys Ser Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg
 645 650 655
 Cys Ile His Ala Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe
 660 665 670
 Asp Lys Cys Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln
 675 680 685
 Ser Gly Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr
 690 695 700
 Ile Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
 705 710 715 720
 Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser Tyr
 725 730 735
 Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp Val Val
 740 745 750
 Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr Ala Ala Ser
 755 760 765

Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro Leu Thr Leu Gln
770 775 780

Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg Leu Arg Tyr Ser Phe
785 790 795 800

Phe Val Pro Arg Pro Thr Pro Ser Thr Pro Arg Pro Thr Pro Gln Asp
805 810 815

Trp Leu His Arg Arg Ala Gln Ile Leu Glu Ile Leu Arg Arg Arg Pro
820 825 830

Trp Ala Gly Arg Lys
835

<210> 3

<400> 3

000

<210> 4

<211> 26

<212> PRT

<213> Bos taurus

<400> 4

Phe Ala Ser Leu Ser Arg Val Glu Thr Leu Val Val Ala Asp Asp Lys
1 5 10 15

Met Ala Ala Phe His Gly Ala Gly Leu Lys
20 25

<210> 5

<211> 7

<212> PRT

<213> Bos taurus

<400> 5

Tyr Thr Gly Val Ala Pro Arg
1 5

<210> 6

<211> 11

<212> PRT

<213> Bos taurus

<400> 6

Ala Leu Gly Tyr Tyr Tyr Val Leu Asp Pro Arg
1 5 10

<210> 7

<211> 21

<212> DNA

<213> Mus musculus

<400> 7

gggggtggtg tccagttctc c

21

<210> 8

<211> 23

<212> DNA

<213> Mus musculus

<400> 8

ggccctggaa agctcttgaa gag

23

C1
<210> 9

<211> 23

<212> DNA

<213> Homo sapiens

<400> 9

ccccggaatg gtggcaagta ctg

23

<210> 10

<211> 23

<212> DNA

<213> Homo sapiens

<400> 10

accacatct gtctgactcc aaa

23

<210> 11

<211> 23

<212> DNA

<213> Homo sapiens

<400> 11
ccagttgggc agtcctcagt gtt 23

<210> 12

<211> 22

<212> DNA

<213> Homo sapiens

<400> 12
ggtcggtgcg gtggtttag gc 22

<210> 13

<211> 17

<212> PRT

<213> Homo sapiens

<400> 13

Cys Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val Ala Asp Asp
1 5 10 15

C1 Lys

<210> 14

<211> 3250

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)..(2910)

<400> 14
tgactcaatc ctgcaagcaa gtgtgtgtgt gtcccatcc cccgcccgt taacttcata 60

gcaaataaca aatacccata aagtcaccagt cgcgcagccc ctccccgcgg gcagcgcact 120

atg ctg ctc ggg tgg gcg tcc ctg ctg ctg tgc gcg ttc cgc ctg ccc 168
Met Leu Leu Gly Trp Ala Ser Leu Leu Leu Cys Ala Phe Arg Leu Pro
1 5 10 15

ctg gcc gcg gtc ggc ccc gcc gcg aca cct gcc cag gat aaa gcc ggg 216
Leu Ala Ala Val Gly Pro Ala Ala Thr Pro Ala Gln Asp Lys Ala Gly
20 25 30

cag cct ccg act gct gca gca gcc gcc cag ccc cgc cgg cgg cag ggg Gln Pro Pro Thr Ala Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly 35 40 45	264
gag gag gtg cag gag cga gcc gag cct ccc ggc cac ccg cac ccc ctg Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu 50 55 60	312
gcg cag cgg cgc agg agc aag ggg ctg gtg cag aac atc gac caa ctc Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu 65 70 75 80	360
tac tcc ggc ggc ggc aag gtg ggc tac ctc gtc tac gcg ggc ggc cgg Tyr Ser Gly Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg 85 90 95	408
agg ttc ctc ttg gac ctg gag cga gat ggt tcg gtg ggc att gct ggc Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly 100 105 110	456
ttc gtg ccc gca gga ggc ggg acg agt gcg ccc tgg cgc cac cgg agc Phe Val Pro Ala Gly Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser 115 120 125	504
cac tgc ttc tat cgg ggc aca gtg gac gct agt ccc cgc tct ctg gct His Cys Phe Tyr Arg Gly Thr Val Asp Ala Ser Pro Arg Ser Leu Ala 130 135 140	552
gtc ttt gac ctc tgt ggg ggt ctc gac ggc ttc ttc gcg gtc aag cac Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His 145 150 155 160	600
gcg cgc tac acc cta aag cca ctg ctg cgc gga ccc tgg gcg gag gaa Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu 165 170 175	648
gaa aag ggg cgc gtg tac ggg gat ggg tcc gca cgg atc ctg cac gtc Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val 180 185 190	696
tac acc cgc gag ggc ttc agc ttc gag gcc ctg ccg ccg cgc gcc agc Tyr Thr Arg Glu Gly Phe Ser Phe Glu Ala Leu Pro Pro Arg Ala Ser 195 200 205	744
tgc gaa acc ccc gcg tcc aca ccg gag gcc cac gag cat gct ccg gcg Cys Glu Thr Pro Ala Ser Thr Pro Glu Ala His Glu His Ala Pro Ala 210 215 220	792
cac agc aac ccg agc gga cgc gca gca ctg gcc tcg cag ctc ttg gac His Ser Asn Pro Ser Gly Arg Ala Ala Leu Ala Ser Gln Leu Leu Asp 225 230 235 240	840
cag tcc gct ctc tcg ccc gct ggg ggc tca gga ccg cag acg tgg tgg Gln Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp 245 250 255	888

C1

cgg cgg cgg cgc cgc tcc atc tcc cgg gcc cgc cag gtg gag ctg ctt	936
Arg Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu	
260 265 270	
ctg gtg gct gac gcg tcc atg gcg cgg ttg tat ggc cgg ggc ctg cag	984
Leu Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln	
275 280 285	
cat tac ctg ctg acc ctg gcc tcc atc gcc aat agg ctg tac agc cat	1032
His Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His	
290 295 300	
gct agc atc gag aac cac atc cgc ctg gcc gtg gtg aag gtg gtg gtg	1080
Ala Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val	
305 310 315 320	
cta ggc gac aag gac aag agc ctg gaa gtg agc aag aac gct gcc acc	1128
Leu Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr	
325 330 335	
aca ctc aag aac ttt tgc aag tgg cag cac caa cac aac cag ctg gga	1176
Thr Leu Lys Asn Phe Cys Lys Trp Gln His Gln His Asn Gln Leu Gly	
340 345 350	
gat gac cat gag gag cac tac gat gca gct atc ctg ttt act cgg gag	1224
Asp Asp His Glu Glu His Tyr Asp Ala Ala Ile Leu Phe Thr Arg Glu	
355 360 365	
gat tta tgt ggg cat cat tca tgt gac acc ctg gga atg gca gac gtt	1272
Asp Leu Cys Gly His His Ser Cys Asp Thr Leu Gly Met Ala Asp Val	
370 375 380	
ggg acc ata tgt tct cca gag cgc agc tgt gct gtg att gaa gac gat	1320
Gly Thr Ile Cys Ser Pro Glu Arg Ser Cys Ala Val Ile Glu Asp Asp	
385 390 395 400	
ggc ctc cac gca gcc ttc act gtg gct cac gaa atc gga cat tta ctt	1368
Gly Leu His Ala Ala Phe Thr Val Ala His Glu Ile Gly His Leu Leu	
405 410 415	
ggc ctc tcc cat gac gat tcc aaa ttc tgt gaa gag acc ttt ggt tcc	1416
Gly Leu Ser His Asp Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser	
420 425 430	
aca gaa gat aag cgc tta atg tct tcc atc ctt acc agc att gat gca	1464
Thr Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala	
435 440 445	
tct aag ccc tgg tcc aaa tgc act tca gcc acc atc aca gaa ttc ctg	1512
Ser Lys Pro Trp Ser Lys Cys Thr Ser Ala Thr Ile Thr Glu Phe Leu	
450 455 460	
gat gat ggc cat ggt aac tgt ttg ctg gac cta cca cga aag cag atc	1560
Asp Asp Gly His Gly Asn Cys Leu Leu Asp Leu Pro Arg Lys Gln Ile	
465 470 475 480	
ctg ggc ccc gaa gaa ctc cca gga cag acc tac gat gcc acc cag cag	1608

C

Leu Gly Pro Glu Glu Leu Pro Gly Gln Thr Tyr Asp Ala Thr Gln Gln
 485 490 495

tgc aac ctg aca ttc ggg cct gag tac tcc gtg tgt ccc ggc atg gat 1656
 Cys Asn Leu Thr Phe Gly Pro Glu Tyr Ser Val Cys Pro Gly Met Asp
 500 505 510

gtc tgt gct cgc ctg tgg tgt gct gtg gta cgc cag ggc cag atg gtc 1704
 Val Cys Ala Arg Leu Trp Cys Ala Val Val Arg Gln Gly Gln Met Val
 515 520 525

tgt ctg acc aag aag ctg cct gcg gtg gaa ggg acg cct tgt gga aag 1752
 Cys Leu Thr Lys Lys Leu Pro Ala Val Glu Gly Thr Pro Cys Gly Lys
 530 535 540

ggg aga atc tgc ctg cag ggc aaa tgt gtg gac aaa acc aag aaa aaa 1800
 Gly Arg Ile Cys Leu Gln Gly Lys Cys Val Asp Lys Thr Lys Lys Lys
 545 550 555 560

tat tat tca acg tca agc cat ggc aac tgg gga tct tgg gga tcc tgg 1848
 Tyr Tyr Ser Thr Ser Ser His Gly Asn Trp Gly Ser Trp Gly Ser Trp
 565 570 575

ggc cag tgt tct cgc tca tgt gga gga gga gtg cag ttt gcc tat cgt 1896
 Gly Gln Cys Ser Arg Ser Cys Gly Gly Gly Val Gln Phe Ala Tyr Arg
 580 585 590

cac tgt aat aac cct gct ccc aga aac aac gga cgc tac tgc aca ggg 1944
 His Cys Asn Asn Pro Ala Pro Arg Asn Asn Gly Arg Tyr Cys Thr Gly
 595 600 605

aag agg gcc atc tac cgc tcc tgc agt ctc atg ccc tgc cca ccc aat 1992
 Lys Arg Ala Ile Tyr Arg Ser Cys Ser Leu Met Pro Cys Pro Pro Asn
 610 615 620

ggt aaa tca ttt cgt cat gaa cag tgt gag gcc aaa aat ggc tat cag 2040
 Gly Lys Ser Phe Arg His Glu Gln Cys Glu Ala Lys Asn Gly Tyr Gln
 625 630 635 640

tct gat gca aaa gga gtc aaa act ttt gtg gaa tgg gtt ccc aaa tat 2088
 Ser Asp Ala Lys Gly Val Lys Thr Phe Val Glu Trp Val Pro Lys Tyr
 645 650 655

gca ggt gtc ctg cca gcg gat gtg tgc aag ctg acc tgc aga gcc aag 2136
 Ala Gly Val Leu Pro Ala Asp Val Cys Lys Leu Thr Cys Arg Ala Lys
 660 665 670

ggc act ggc tac tat gtg gta ttt tct cca aag gtg acc gat ggc act 2184
 Gly Thr Gly Tyr Tyr Val Val Phe Ser Pro Lys Val Thr Asp Gly Thr
 675 680 685

gaa tgt agg ccg tac agt aat tcc gtc tgc gtc cgg ggg aag tgt gtg 2232
 Glu Cys Arg Pro Tyr Ser Asn Ser Val Cys Val Arg Gly Lys Cys Val
 690 695 700

aga act ggc tgt gac ggc atc att ggc tca aag ctg cag tat gac aag 2280
 Arg Thr Gly Cys Asp Gly Ile Ile Gly Ser Lys Leu Gln Tyr Asp Lys

705	710	715	720	
tgc gga gta tgt gga gga gac aac tcc agc tgt aca aag att gtt gga				2328
Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys Thr Lys Ile Val Gly	725	730	735	
acc ttt aat aag aaa agt aag ggt tac act gac gtg gtg agg att cct				2376
Thr Phe Asn Lys Lys Ser Lys Gly Tyr Thr Asp Val Val Arg Ile Pro	740	745	750	
gaa ggg gca acc cac ata aaa gtt cga cag ttc aaa gcc aaa gac cag				2424
Glu Gly Ala Thr His Ile Lys Val Arg Gln Phe Lys Ala Lys Asp Gln	755	760	765	
act aga ttc act gcc tat tta gcc ctg aaa aag aaa aac ggt gag tac				2472
Thr Arg Phe Thr Ala Tyr Leu Ala Leu Lys Lys Lys Asn Gly Glu Tyr	770	775	780	
ctt atc aat gga aag tac atg atc tcc act tca gag act atc att gac				2520
Leu Ile Asn Gly Lys Tyr Met Ile Ser Thr Ser Glu Thr Ile Ile Asp	785	790	795	800
atc aat gga aca gtc atg aac tat agc ggt tgg agc cac agg gat gac				2568
Ile Asn Gly Thr Val Met Asn Tyr Ser Gly Trp Ser His Arg Asp Asp	805	810	815	
ttc ctg cat ggc atg ggc tac tct gcc acg aag gaa att cta ata gtg				2616
Phe Leu His Gly Met Gly Tyr Ser Ala Thr Lys Glu Ile Leu Ile Val	820	825	830	
cag att ctt gca aca gac ccc act aaa cca tta gat gtc cgt tat agc				2664
Gln Ile Leu Ala Thr Asp Pro Thr Lys Pro Leu Asp Val Arg Tyr Ser	835	840	845	
ttt ttt gtt ccc aag aag tcc act cca aaa gta aac tct gtc act agt				2712
Phe Phe Val Pro Lys Lys Ser Thr Pro Lys Val Asn Ser Val Thr Ser	850	855	860	
cat ggc agc aat aaa gtg gga tca cac act tcg cag ccg cag tgg gtc				2760
His Gly Ser Asn Lys Val Gly Ser His Thr Ser Gln Pro Gln Trp Val	865	870	875	880
acg ggc cca tgg ctc gcc tgc tct agg acc tgt gac aca ggt tgg cac				2808
Thr Gly Pro Trp Leu Ala Cys Ser Arg Thr Cys Asp Thr Gly Trp His	885	890	895	
acc aga acg gtg cag tgc cag gat gga aac cgg aag tta gca aaa gga				2856
Thr Arg Thr Val Gln Cys Gln Asp Gly Asn Arg Lys Leu Ala Lys Gly	900	905	910	
tgt cct ctc tcc caa agg cct tct gcg ttt aag caa tgc ttg ttg aag				2904
Cys Pro Leu Ser Gln Arg Pro Ser Ala Phe Lys Gln Cys Leu Leu Lys	915	920	925	
aaa tgt tagcctgtgg ttatgatctt atgcacaaag ataactggag gattcagcac				2960
Lys Cys	930			

C1

cgatgcagtc gtggtgaaca ggaggtctac ctaacgcaca gaaagtcatg cttcagtgac 3020
 attgtcaaca ggagtccaat tatgggcaga atctgctctc tgtgaccaa agaggatgtg 3080
 cactgcttca cgtgacagtg gtgaccttgc aatatagaaa aacttgggag ttattgaaca 3140
 tccctggga ttacaagaaa cactgatgaa tggttaaata ggggacattt gaagatggca 3200
 gaactgtctc ccccttgta cctacctctg aatagaatgt ctttaatggt 3250

<210> 15

<211> 930

<212> PRT

<213> Homo sapiens

<400> 15

Met Leu Leu Gly Trp Ala Ser Leu Leu Leu Cys Ala Phe Arg Leu Pro
 1 5 10 15

Leu Ala Ala Val Gly Pro Ala Ala Thr Pro Ala Gln Asp Lys Ala Gly
 20 25 30

Gln Pro Pro Thr Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly
 35 40 45

Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu
 50 55 60

Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu
 65 70 75 80

Tyr Ser Gly Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg
 85 90 95

Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly
 100 105 110

Phe Val Pro Ala Gly Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser
 115 120 125

His Cys Phe Tyr Arg Gly Thr Val Asp Ala Ser Pro Arg Ser Leu Ala
 130 135 140

Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His
 145 150 155 160

Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu
 165 170 175

Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val
 180 185 190

C1

Tyr Thr Arg Glu Gly Phe Ser Phe Glu Ala Leu Pro Pro Arg Ala Ser
 195 200 205
 Cys Glu Thr Pro Ala Ser Thr Pro Glu Ala His Glu His Ala Pro Ala
 210 215 220
 His Ser Asn Pro Ser Gly Arg Ala Ala Leu Ala Ser Gln Leu Leu Asp
 225 230 235 240
 Gln Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp
 245 250 255
 Arg Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu
 260 265 270
 Leu Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln
 275 280 285
 His Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His
 290 295 300
 Ala Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val
 305 310 315 320
 Leu Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr
 325 330 335
 Thr Leu Lys Asn Phe Cys Lys Trp Gln His Gln His Asn Gln Leu Gly
 340 345 350
 Asp Asp His Glu Glu His Tyr Asp Ala Ala Ile Leu Phe Thr Arg Glu
 355 360 365
 Asp Leu Cys Gly His His Ser Cys Asp Thr Leu Gly Met Ala Asp Val
 370 375 380
 Gly Thr Ile Cys Ser Pro Glu Arg Ser Cys Ala Val Ile Glu Asp Asp
 385 390 395 400
 Gly Leu His Ala Ala Phe Thr Val Ala His Glu Ile Gly His Leu Leu
 405 410 415
 Gly Leu Ser His Asp Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser
 420 425 430
 Thr Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala
 435 440 445
 Ser Lys Pro Trp Ser Lys Cys Thr Ser Ala Thr Ile Thr Glu Phe Leu
 450 455 460
 Asp Asp Gly His Gly Asn Cys Leu Leu Asp Leu Pro Arg Lys Gln Ile
 465 470 475 480
 Leu Gly Pro Glu Glu Leu Pro Gly Gln Thr Tyr Asp Ala Thr Gln Gln
 485 490 495

Cys Asn Leu Thr Phe Gly Pro Glu Tyr Ser Val Cys Pro Gly Met Asp
 500 505 510
 Val Cys Ala Arg Leu Trp Cys Ala Val Val Arg Gln Gly Gln Met Val
 515 520 525
 Cys Leu Thr Lys Lys Leu Pro Ala Val Glu Gly Thr Pro Cys Gly Lys
 530 535 540
 Gly Arg Ile Cys Leu Gln Gly Lys Cys Val Asp Lys Thr Lys Lys Lys
 545 550 555 560
 Tyr Tyr Ser Thr Ser Ser His Gly Asn Trp Gly Ser Trp Gly Ser Trp
 565 570 575
 Gly Gln Cys Ser Arg Ser Cys Gly Gly Gly Val Gln Phe Ala Tyr Arg
 580 585 590
 His Cys Asn Asn Pro Ala Pro Arg Asn Asn Gly Arg Tyr Cys Thr Gly
 595 600 605
 Lys Arg Ala Ile Tyr Arg Ser Cys Ser Leu Met Pro Cys Pro Pro Asn
 610 615 620
 Gly Lys Ser Phe Arg His Glu Gln Cys Glu Ala Lys Asn Gly Tyr Gln
 625 630 635 640
 Ser Asp Ala Lys Gly Val Lys Thr Phe Val Glu Trp Val Pro Lys Tyr
 645 650 655
 Ala Gly Val Leu Pro Ala Asp Val Cys Lys Leu Thr Cys Arg Ala Lys
 660 665 670
 Gly Thr Gly Tyr Tyr Val Val Phe Ser Pro Lys Val Thr Asp Gly Thr
 675 680 685
 Glu Cys Arg Pro Tyr Ser Asn Ser Val Cys Val Arg Gly Lys Cys Val
 690 695 700
 Arg Thr Gly Cys Asp Gly Ile Ile Gly Ser Lys Leu Gln Tyr Asp Lys
 705 710 715 720
 Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys Thr Lys Ile Val Gly
 725 730 735
 Thr Phe Asn Lys Lys Ser Lys Gly Tyr Thr Asp Val Val Arg Ile Pro
 740 745 750
 Glu Gly Ala Thr His Ile Lys Val Arg Gln Phe Lys Ala Lys Asp Gln
 755 760 765
 Thr Arg Phe Thr Ala Tyr Leu Ala Leu Lys Lys Lys Asn Gly Glu Tyr
 770 775 780
 Leu Ile Asn Gly Lys Tyr Met Ile Ser Thr Ser Glu Thr Ile Ile Asp
 785 790 795 800

C1

Ile Asn Gly Thr Val Met Asn Tyr Ser Gly Trp Ser His Arg Asp Asp
805 810 815

Phe Leu His Gly Met Gly Tyr Ser Ala Thr Lys Glu Ile Leu Ile Val
820 825 830

Gln Ile Leu Ala Thr Asp Pro Thr Lys Pro Leu Asp Val Arg Tyr Ser
835 840 845

Phe Phe Val Pro Lys Lys Ser Thr Pro Lys Val Asn Ser Val Thr Ser
850 855 860

His Gly Ser Asn Lys Val Gly Ser His Thr Ser Gln Pro Gln Trp Val
865 870 875 880

Thr Gly Pro Trp Leu Ala Cys Ser Arg Thr Cys Asp Thr Gly Trp His
885 890 895

Thr Arg Thr Val Gln Cys Gln Asp Gly Asn Arg Lys Leu Ala Lys Gly
900 905 910

Cys Pro Leu Ser Gln Arg Pro Ser Ala Phe Lys Gln Cys Leu Leu Lys
915 920 925

Lys Cys
930

<210> 16

<211> 42

<212> PRT

<213> Homo sapiens

<400> 16

Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu Leu Val Ala Asp Ala
1 5 10 15

Ser Met Ala Arg Met Tyr Gly Arg Gly Leu Gln His Tyr Leu Leu Thr
20 25 30

Leu Ala Ser Ile Ala Asn Lys Leu Tyr Phe
35 40

<210> 17

<211> 23

<212> DNA

<213> Mus musculus

<400> 17

cggccacgac cctcaagaac ttt

<210> 18

<211> 25

<212> DNA

<213> Mus musculus

<400> 18

gcatggaggc catcatcttc aatca

25

<210> 19

<211> 22

<212> DNA

<213> Homo sapiens

<400> 19

gggaggattt atgtgggcat ca

22

<210> 20

<211> 23

<212> DNA

<213> Homo sapiens

<400> 20

gtgcatttgg accagggctt aga

23

<210> 21

<211> 13

<212> PRT

<213> artificial

<220>

<223> Synthesized peptide.

<220>

<221> MOD_RES

<222> (12)..(12)

<223> Acp

<400> 21

Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu Xaa Cys

1

5

(-20)

C1